

Figure 1A

1 CCCACGCGTCCGATTAAAGTCAGGAGAGAGCTACAACCAAGTAAGCAAGTGTGTCAGGGCTC 60  
 61 ACCAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTGTTCCTCAA 120  
 1 M O G O G R R R G T C K D I F C S K 18  
 121 AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTG 180  
 19 M A S Y L Y G V L F A V G L C A P I Y C 38  
 181 TGTGTCCCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCC 240  
 39 V S P A N A P S A Y P R P S S T K S T P 58  
 241 TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT 300  
 59 A S Q V Y S L N T D F A F R L Y R R L V 78  
 301 TTTGGAGACCCCGAGTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGC 360  
 79 L E T P S Q N I F F S P V S V S T S L A 98  
 361 CATGCTCTCCCTTGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTT 420  
 99 M L S L G A H S V T K T Q I L Q G L G F 118  
 421 CAACCTCACACACACACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTC 480  
 119 N L T H T P E S A I H Q G F Q H L V H S 138  
 481 ACTGACTGTTCCCAGCAAAGACCTGACCTTGAAGATGGGAAGTGGCCTCTTCGTCAAGAA 540  
 139 L T V P S K D L T L K M G S A L F V K K 158  
 541 GGAGCTGCAGCTGCAGGCAAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGT 600  
 159 E L Q L Q A N F L G N V K R L Y E A E V 178  
 601 CTTTCTACAGATTTCTCCAACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAA 660  
 179 F S T D F S N P S I A Q A R I N S H V K 198  
 661 AAAGAAGACCCAAGGGAAGGTTGTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCAT 720  
 199 K K T Q G K V V D I I Q G L D L L T A M 218  
 721 GGTCTGGTGAATCACATTTTCTTTAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATA 780  
 219 V L V N H I F F K A K W E K P F H L E Y 238  
 781 TACAAGAAAGAACTTCCCATTCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT 840  
 239 T R K N F P F L V G E Q V T V Q V P M M 258  
 841 GCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGCTGAACTGCTTTGTGCTGCA 900  
 259 H Q K E Q F A F G V D T E L N C F V L Q 278

Figure 1B

901 GATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCCTCCCTAGCAAGGGCAAGATGAG 960  
 279 M D Y K G D A V A F F V L P S K G K M R 298  
  
 961 GCAACTGGAACAGGCCTTGTTCAGCCAGAACACTGATAAAGTGGAGCCACTCACTCCAGAA 1020  
 299 Q L E Q A L S A R T L I K W S H S L Q K 318  
  
 1021 AAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCCATTTCTGCCTCCTACAATCTGGAAAC 1080  
 319 R W I E V F I P R F S I S A S Y N L E T 338  
  
 1081 CATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAAATGCTGATTTTTCTGGAAT 1140  
 339 I L P K M G I Q N A F D K N A D F S G I 358  
  
 1141 TGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATGTCAG 1200  
 359 A K R D S L Q V S K A T H K A V L D V S 378  
  
 1201 TGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGGA 1260  
 379 E E G T E A T A A T T T K F I V **R S** K D 398  
  
 1261 TGGTCCCTCTTACTTCACCTGTCTCCTTCAATAGGACCTTCCTGATGATGATTACAAATAA 1320  
 399 G P S Y F T **V S E N R T E I V S** T N K 418  
  
 1321 AGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAAATCCCACTAAATCCTAGGTGGG 1380  
 419 A T D G I L F L G K V E N P T K S \* 436  
  
 1381 AAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCT 1440  
  
 1441 CTTTCTGTCTGAGGGTGCATTTGACCCCAGTGAGCTGGATTTCGCTGGCAGGGATGCCA 1500  
  
 1501 CTTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCCAGTCACAAGCCAACACCCATT 1560  
  
 1561 AACCCCAGTCAGTGCCCTTTTCCACAAATTCTCCCAGGTAACTAGCTTCATGGGATGTTG 1620  
  
 1621 CTGGGTTACCATATTTCCATTCTTGGGGCTCCCAGGAATGGAAATACGCCAACCAGGT 1680  
  
 1681 TAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAAAAAA 1740  
  
 1741 AAAAAAAAAAAAAAAAAAAAAAAAAA 1766

Figure 2

		1		50
AL132708_FL	(1)	MQQGRRRGTCCKDIFCSKMASYLYGV	FAVGLCAPIYCVSPANAPSAYPR	
AACT_HUMAN	(1)	-----	MERMLPPLALGLLAAGFCPAVLCHPNSPLD	
KAIN_HUMAN	(1)	-----	MHLIDYLLLLVGLLALSHGQLHVEHDGESCS	
THBG_HUMAN	(1)	-----	MSPFLYLVLVLGLHATIHCAASPEGKVTACHS	
		51		100
AL132708_FL	(51)	PS-----	STKSTPASQVYSLNTDFAERLYRRLVLET	PSQNIFFSPVSV
AACT_HUMAN	(31)	EENLTQENQDRGTHVDLGLASANVDFAESLYKQLVLKAPDKNVIFSPLSI		
KAIN_HUMAN	(33)	NSSHQQILETGEQSPSLKIAPANADFAERFYLIASETPGKNIFFSPLSI		
THBG_HUMAN	(33)	-----	SQPNATLYKMSSINADFAENLYRRFTVET	PDKNIFFSPVSI
		101		150
AL132708_FL	(94)	STSLAMLSLGAHSVTKTQTLQGLGFNLTHTPESAIHQGFQHLVHSLTVPS		
AACT_HUMAN	(81)	STALAFSLSLGAHNTTLTETLKGLKFNLTETSEAEIHQSFOHLLRTLNQSS		
KAIN_HUMAN	(83)	SAAYAMLSLGACSHSRSQLLEGLGFNLTELSQDVHRGFQHLHTLNLPG		
THBG_HUMAN	(74)	SAALVMLSFGACCSTQTEIVETLGFNLTDTPMVEIQHGFQHLICSLNFPK		
		151		200
AL132708_FL	(144)	KDITLKMGSALFVKKEQLQANFLGNVKRLYEAVEFSTDFSNPSIAQART		
AACT_HUMAN	(131)	DELQLSMGNAMFVKEQLSLLDRETEDAKRLYGSEAFATDFQDSAAAKKL		
KAIN_HUMAN	(133)	HGLETRVGSALFLSHNLKFLAKFLNDTMAVVEAKLPHINFYDTVGTIQL		
THBG_HUMAN	(124)	KELELQIGNALFQKHFKPLAKFLNDVKTLVETEVESTDFSNISAAKQET		
		201		250
AL132708_FL	(194)	NSHVKKKTQGGVVDIIQGLDLLTAMVLVNHFFKAKWEKPEHLEYTRKNF		
AACT_HUMAN	(181)	NDYVKNGTIRGKITDLIKDLSQTMVLVNYIFFKAKWEMPFDPQDTHQSR		
KAIN_HUMAN	(183)	NDHVKKETRGKIVDLVSELKKDVLVNLVNYTFKALWEKPEFISSRTTPKD		
THBG_HUMAN	(174)	NSHVEMQTKGKVVGLIQDLKPNITMVLVNYTHEKAWANPEDPSTEDSS		
		251		300
AL132708_FL	(244)	PFLVGEQVTVQVPMHMQKEQFAFGVDTELNCFVLQMDYKGDVAVAFVLP		
AACT_HUMAN	(231)	FYLSKKKWVMVPMMSLHHLTIPYFRDEESCTVVELKYTGNASALFILPD		
KAIN_HUMAN	(233)	FYVDENTTVRVPMMLQDQEHHWYLDHYLPQSVLRMDYKGDATVFFILPN		
THBG_HUMAN	(224)	SFLIDKTTTVQVPMHMQEQYYHLVDMELNCTVLQMDYSKNALALFVLPK		
		301		350
AL132708_FL	(294)	KGKMRQLEQALSARTLIKWSHSTQKR----	WIEVFIPRFSTISASYNLETI	
AACT_HUMAN	(281)	QDKMEEVEAMLLPETIKRWRDSLEFR---	EIGELYLPKFSTISRDNINDI	
KAIN_HUMAN	(283)	QGKMRREIEVLTPEMIMRWNNLLRKRNFYKKLEHLHPKFSTISGSYVLDQI		
THBG_HUMAN	(274)	EGMESVEAAMSSKTLKKWNRLQKG----	WVDLFVPKFSTISATYDLGAT	
		351		400
AL132708_FL	(340)	LPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT		
AACT_HUMAN	(328)	LLQLGIEEAFTSKADLSGITGARNLAVSQVVHKAVLDVFEETEAASAATA		
KAIN_HUMAN	(333)	LPRLGFTDLFSKWADLSGITKQKLEASKSFHKATLDVDEAGTEAAAATT		
THBG_HUMAN	(320)	LLKMGIQHAYSENADFSGLTEDNGLKLSNAAHKAVLHIGKEGTEAAAVPE		
		401	↓↓↓↓↓↓↓↓↓↓	446
AL132708_FL	(390)	TKFIVRSKDGPSYFTVSFNTFLMNTNKATDGILELGGKVENPTKS		
AACT_HUMAN	(378)	VKITLLSALVETRTIVRFNRPFLMITVPTDTQNIFFEMSKVTNPKQA		
KAIN_HUMAN	(383)	FAIKFFSAQTN-RHILRFNRPFLVVFSTSTQSVLELGGKVVDPTKP		
THBG_HUMAN	(370)	VELSDQENTFLHPIIQIDRSFMLLTLERSIRSILELGGKVNPTEA		

Figure 3

LSI-01	MQGQRRRGRT CKDIFCSKMA SYLYGVLFV GLCAPIYCVS PANAPSAYPR
pdb1qlp	..... MDPQ GDAAQKTDTS
LSI-01	PSSTKSTPAS QVYSLNTDFA FRLYRRLVLE TPSQNIFFSP VSVSTSLAML
pdb1qlp	HHDQDHPTFN KITPNLAEPF FSLYRQLAHQ SNSTNIFFSP VSIATAFAMI
LSI-01	SLGAHSVTKT QILQGLGFNL THTPESAIHQ GFQHLVHSLT VPSKDLTKLM
pdb1qlp	SLGTKADTHD ELLEGLNENL TEIPEAQIHE GFQELLRTLN QPDSQLQITT
LSI-01	GSALFVKKEI QIQANFLGNV KRLYEAEVFS TDFSNPSIAQ ARINSHVKKK
pdb1qlp	GNGLFLSEGL KLVDFLEDV KKLHSEAFV VNFQDTEEAQ KQINDYVEKG
LSI-01	TQGVVDIIQ GLDLLTAMVL VNHIFFKAKW EKPFLHLEYTR KNFPFLVGEQ
pdb1qlp	TQGIIVDLVK ELDRDVFAL VNYIFFKGRW ERPFVKDT. EEEDHVDQV
LSI-01	VTQVPMHQ KEQFAFGVDT ELNCFVLQMD YKGDVAFFV LPSKGMROL
pdb1qlp	TTVKVPMKR LGMFNIQHCK KLSSWVLLMK YLGNATAIFF LEDEGLQHL
LSI-01	EQALSARTLI KWSHSLQKRW IEVFIPRFST SASYNLETIL PKMGIONAFD
pdb1qlp	ENELTHDIIT KFLNEDRRS ASLHLEKLSI TGTYDLKSVL GOLGITKVES
LSI-01	KNADFSGIAK RDSLQVSKAT HRAVLDSVEE GTEATAATT KFTVRSKDGF
pdb1qlp	NGADLSGVTE EAPLKLKAV HRAVLTIDEK GTEAAGAMFL EALPMSI..P
LSI-01	S.YFTVSENR TELMMITNKA TDGILFLGKV ENPTKS
pdb1qlp	PE...VKFNK PFVFLMIEQN TKSPLEMGKV VNPTQK

Figure 4.

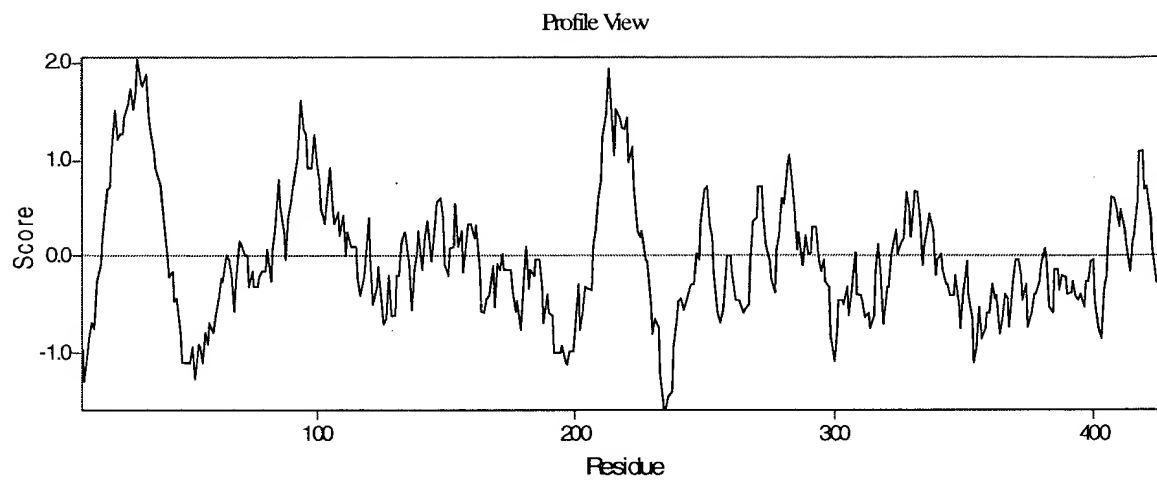
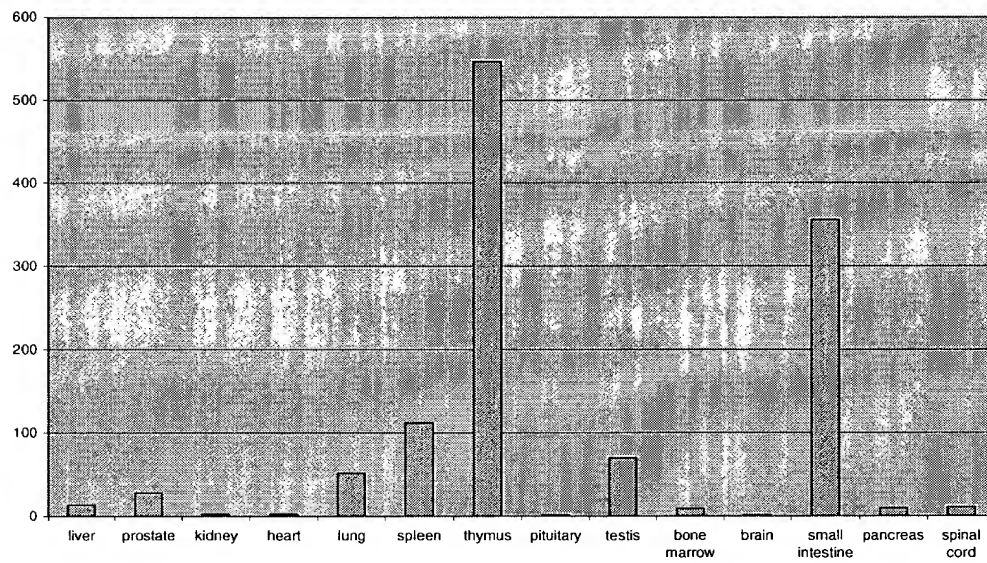
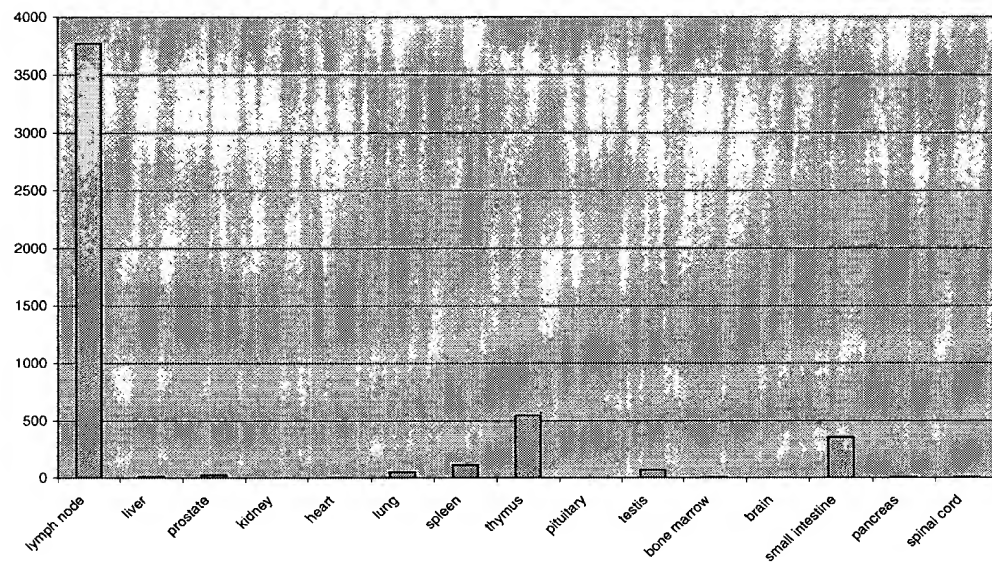


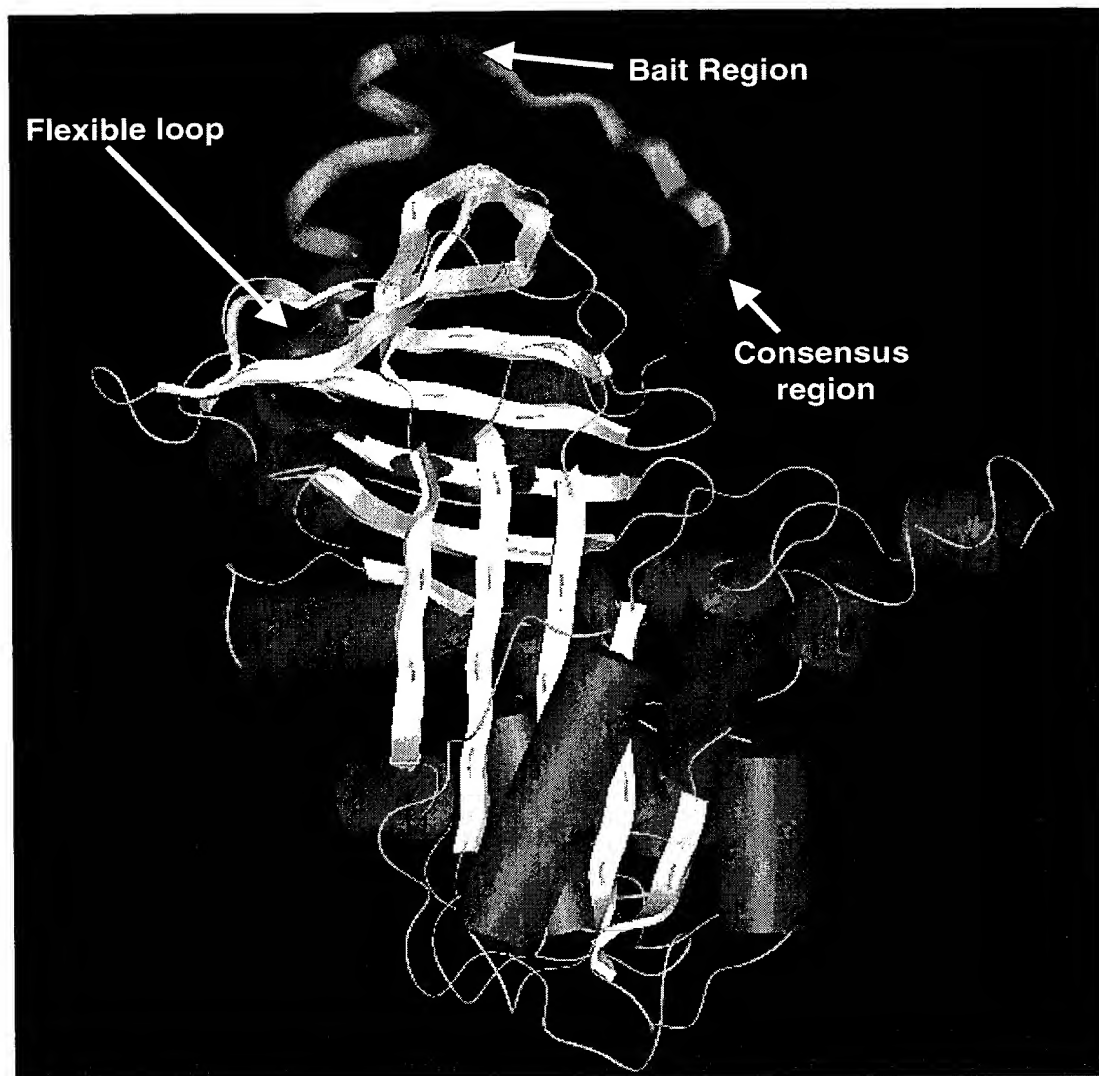
Figure 5.



[illegible]

<b><u>Protein</u></b>	<b><u>Genbank ID</u></b>	<b><u>Identities</u></b>	<b><u>Similarities</u></b>
human $\alpha_1$ -antichymotrypsin	gil112874	46%	52%
human Kallistatin	gil5453888	48%	56%
human thyroxin-binding globulin	gil37142	51%	57%
human $\alpha_1$ -antithrypsin	gil6137432	43%	50%

### Figure 7

[illegible]